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## Phylogenetic Analysis of the Chinese *Rickettsia* Isolate BJ-90

**To the Editor:** Five species of tick-associated rickettsiae have been identified in China; of these, three are human pathogens and two are of unknown pathogenicity (1). In 1990, one isolate, BJ-90, was first obtained from a *Dermacentor sinicus* tick, a newly recognized vector collected in a Beijing suburb, an atypical location for *Rickettsia sibirica* (2). Several taxonomic studies of the phenotype, antigenicity, and genotype of BJ-90 have been performed, with inconsistent results (2-6). Recently, phylogenetic analysis based on several gene comparisons has enabled the phylogenetic classification of this rickettsial species (7-11). To confirm the phylogenetic relationships between the BJ-90 strain and other rickettsiae, the 16S rRNA, *gltA*, and *OmpA* encoding genes were amplified and sequenced. Phylogenetic relationships between the BJ-90 strain and other rickettsia in the GenBank database were inferred by the parsimony and neighbor-joining methods (9). Bootstrap analyses were used to assess the reliability of the phylogenetic analysis.

Both methods showed a high degree of similarity between BJ-90, *R. sibirica* and "*R. mongolotimonae*," which were grouped in the same cluster in three inferred dendrograms. The data from the 16S rRNA and *gltA* sequences showed low statistical significance in the cluster (bootstrap values for the nodes 50% and 33%, respectively). However, data from the *ompA* gene sequence showed highly significant similarity in the cluster (bootstrap value 100%), confirming the reliability of the phylogenetic analysis. The results of this phylogenetic analysis are consistent with those of previous phenotypic, genotypic, and phylogenetic analyses (2,3,5-11), as well as taxonomy derived from direct antigenic comparison of the species (4). The sequences of 16S rRNA, *gltA*, and *OmpA* have been assigned the following GenBank accession numbers: AF178036 for 16S rRNA, AF178035 for *gltA*, AF179365 for the 611-bp sequence of *ompA*, and AF179367 for the 3174-bp sequence of *ompA*. According to previous genotypic and antigenic studies and our phylogenetic analysis, in which the BJ-90 strain is closer to *R. sibirica* than *R. mongolotimonae* in the dendrogram inferred from comparison of the *ompA* encoding gene sequences, the BJ-90 strain should be considered a variant of *R. sibirica*.

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